AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions and listings of claims in the present application:

Claims 1-9 **(Canceled)**

10. **(Currently Amended)** A method of analyzing a modification in a DNA to be assayed, said method comprising the steps of:

(1) preparing a mixture of DNA fragments ~~in which a modified base or a base is exposed,~~ from the DNA to be assayed, said preparing comprising either:

(a) digesting genomic DNA with a restriction enzyme to generate a mixture of DNA fragments having cohesive ends containing a base or a modified base, wherein said restriction enzyme is effective to digest DNA at its recognition site in both the presence and absence of a modification in said recognition site, and wherein the genomic DNA is prepared from a biological sample and pretreated with a nuclease capable of digesting a single-stranded DNA before digesting the genomic DNA with the restriction enzyme, or

(b) fragmenting genomic DNA and rendering the fragmented genomic DNAs fully or partially single-stranded to generate a mixture of single-stranded DNA fragments or partially single-stranded DNA fragments in which a modified base or a base is exposed in the single-stranded region, wherein the genomic DNA or the fragmented genomic DNAs are prepared from a biological sample and pretreated with a nuclease capable of digesting a single-stranded DNA before rendering the fragmented genomic DNAs fully or partially single-stranded;

(2) bringing the mixture of DNA fragments obtained in ~~the~~ method step (1) into contact with either an antibody specific to the modified base or an antibody specific to the base that is not modified [[,]] and separating the mixture into ~~a group consisting of~~ the following:

(a) a group of DNA fragments which form an immunocomplex with the antibody and another group ~~consisting~~ of DNA fragments which do not react with the antibody, or

(b) a group ~~consisting~~ of DNA fragments showing a high affinity for the antibody and another group ~~consisting~~ of DNA fragments showing a low affinity for the antibody, and

(3) analyzing all or part of the DNA fragments contained in each of the DNA fragment groups with a DNA array to determine whether the DNA assayed includes a modification.

~~, wherein the mixture of DNA fragments prepared in step (1) is~~

~~(a) a mixture of DNA fragments in which a modified base or a base is exposed at a cohesive end thereof, obtained by digesting genomic DNA with a restriction enzyme which can digest a DNA regardless of the presence or absence of a modification in a recognition site to generate a cohesive end containing a modified base or a base, wherein the genomic DNA is prepared from a biological sample and pretreated with a nuclease capable of digesting a single-stranded DNA, before digesting the genomic DNA with the restriction enzyme, or~~

~~(b) a mixture of single-stranded DNA fragments or partially single-stranded DNA fragments in which a modified base or a base is exposed in the single-stranded region, obtained by fragmenting genomic DNA and rendering the fragmented genomic DNAs fully or partially single-stranded, wherein the genomic DNA or the fragmented genomic DNAs are prepared from a biological sample~~

~~and pretreated with a nuclease capable of digesting a single-stranded DNA, before rendering the fragmented genomic DNAs fully or partially single-stranded.~~

Claims 11-20 **(Canceled)**

21. **(New)** A method of analyzing a modification in a DNA to be assayed, said method comprising the steps of:

(1) preparing a mixture of DNA fragments from the DNA to be assayed, said preparing comprising either:

(a) digesting genomic DNA with a restriction enzyme to generate a mixture of DNA fragments having cohesive ends containing a base or a modified base, wherein said restriction enzyme is effective to digest DNA at its recognition site in both the presence and absence of a modification in said recognition site, wherein said modification is a methylation, and wherein the genomic DNA is prepared from a biological sample and pretreated with a nuclease capable of digesting a single-stranded DNA before digesting the genomic DNA with the restriction enzyme, or

(b) fragmenting genomic DNA and rendering the fragmented genomic DNAs fully or partially single-stranded to generate a mixture of single-stranded DNA fragments or partially single-stranded DNA fragments in which a modified base or a base is exposed in the single-stranded region, wherein the genomic DNA or the fragmented genomic DNAs are prepared from a biological sample and pretreated with a nuclease capable of digesting a single-stranded DNA before rendering the fragmented genomic DNAs fully or partially single-stranded;

(2) bringing the mixture of DNA fragments obtained in method step (1) into contact with either an antibody specific to the modified base or an antibody specific to the base that is not modified and separating the mixture into the following:

(a) a group of DNA fragments which form an immunocomplex with the antibody and another group of DNA fragments which do not react with the antibody, or

(b) a group of DNA fragments showing a high affinity for the antibody and another group of DNA fragments showing a low affinity for the antibody, and

(3) analyzing all or part of the DNA fragments contained in each of the DNA fragment groups with a DNA array to determine whether the DNA assayed includes a modification, wherein said modification is a methylation.